SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Lal, Preeti
Shah, Purvi

(ii) TITLE OF THE INVENTION: NEW HUMAN INTEGRAL MEMBRANE PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0339 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BRAINOT03
(B) CLONE: 662708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Val Lys Ile Ser Phe Gln Pro Ala Val Ala Gly Ile Lys Gly Asp
 1               5                  10                  15
Lys Ala Asp Lys Ala Ser Ala Ser Ala Pro Ala Pro Ala Ser Ala Thr
            20                  25                  30
Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg
        35                  40                  45
Ser Lys Arg Gly Gly Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly
    50                  55                  60
Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr
```

```
65                  70                  75                  80
Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys
                85                  90                  95
Gly Val Leu Tyr Glu Asp Ser Leu Ser Ser Gln Val Arg Thr Gln Met
            100                 105                 110
Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg
        115                 120                 125
Ile Asn Val Pro Val Pro Gln Phe Gly Gly Gly Asp Pro Ala Asp Ile
    130                 135                 140
Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Leu Asp
145                 150                 155                 160
Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro Arg
                165                 170                 175
Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu Pro
            180                 185                 190
Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val Ser
        195                 200                 205
Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly Lys
    210                 215                 220
Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys
225                 230                 235                 240
Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr Phe
                245                 250                 255
Val Val Glu Thr Leu Ile Cys Gly Val Val
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) BRAINOT03
(B) CLONE: 662708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
CGAGCGGGAT CCAAACTTCC GGTGCCTGCA GAGCTCGGAG CGGCGGAGGC AGAGACCGAG      60
GCTGCACCGG CAGAGGCTGC GGGGCGGACG CGCGGGCCGG CGCAGCCATG GTGAAGATTA     120
GCTTCCAGCC CGCCGTGGCT GGCATCAAGG GCGACAAGGC TGACAAGGCG TCGGCGTCGG     180
CCCCTGCGCC GGCCTCGGCC ACCGAGATCC TGCTGACGCC GGCTAGGGAG GAGCAGCCCC     240
CACAACATCG ATCCAAGAGG GGGGGCTCAG TGGGCGGCGT GTGCTACCTG TCGATGGGCA     300
TGGTCGTGCT GCTCATGGGC CTCGTGTTCG CCTCTGTCTA CATCTACAGA TACTTCTTTC     360
TTGCACAGCT GGCCCGAGAT AACTTCTTCC GCTGTGGTGT GCTGTATGAG GACTCCCTGT     420
CCTCCCAGGT CCGGACTCAG ATGGAGCTGG AAGAGGATGT GAAAATCTAC CTCGACGAGA     480
ACTACGAGCG CATCAACGTG CCTGTGCCCC AGTTTGGCGG CGGTGACCCT GCAGACATCA     540
TCCATGACTT CCAGCGGGGT CTGACTGCGT ACCATGATAT CTTGGACAAG TGCTATGTCA     600
TCGAACTCAA CACCACCATT GTGCTGCCCC CTCGCAACTT CTGGGAGCTC CTCATGAACG     660
TGAAGAGGGG GACCTACCTG CCGCAGACGT ACATCATCCA GGAGGAGATG GTGGTCACGG     720
AGCATGTCAG TGACAAGGAG GCCCTGGGGT CCTTCATCTA CCACCTGTGC AACGGGAAAG     780
ACACCTACCG GCTCCGGCGC CGGGCAACGC GGAGGCGGAT CAACAAGCGT GGGGCCAAGA     840
ACTGCAATGC CATCCGCCAC TTCGAGAACA CCTTCGTGGT GGAGACGCTC ATCTGCGGGG     900
TGGTGTGAGG CCCTCCTCCC CCAGAACCCC CTGCCGTGTT CCTCTTTTCT TCTTTCCGGC     960
TGCTCTCTGG CCCTCCTCCT TCCCCCTGCT TAGCTTGTAC TTTGGACGCG TTTCTATAGA    1020
GGTGACATGT CTCTCCATTC CTCTCCAACC CTGCCCACCT CCCTGTACCA GAGCTGTGAT    1080
CTCTCGGTGG GGGGCCCATC TCTGCTGACC TGGGTGTGGC GGAGGGAGAG GCGATGCTGC    1140
AAAGTGTTTT CTGTGTCCCA CTGTCTTGAA GCTGGGCCTG C                        1181
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 624778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
 1               5                  10                  15
Ala Arg Gln Asp Ile Glu Ala Leu Val Ser Arg Thr Val Arg Ala Gln
            20                  25                  30
Ile Leu Thr Gly Lys Glu Leu Arg Val Val Pro Gln Glu Lys Asp Gly
        35                  40                  45
Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu
    50                  55                  60
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
65                  70                  75                  80
Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Glu Asp
                85                  90                  95
Pro Val Asn Ser Ile Pro Gly Gly Glu Pro Tyr Phe Leu Pro Val Thr
            100                 105                 110
Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
        115                 120                 125
Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
    130                 135                 140
Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
145                 150                 155                 160
Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Thr Pro Lys Asn Leu
                165                 170                 175
Val Glu Leu Phe Gly Lys Leu Ala Ser Gly Lys Tyr Leu Pro His Thr
            180                 185                 190
Tyr Val Val Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val
        195                 200                 205
Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
    210                 215                 220
Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
225                 230                 235                 240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
                245                 250                 255
Glu Thr Lys Ile Cys Gln Glu
            260
```